10/777,288

<!--StartFragment--> GenCore version 5.1.9

Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 3, 2006, 14:02:40; Search time 7317 Seconds

(without alignments)

11247.824 Million cell updates/sec

Title: US-10-777-288A-899

Perfect score: 1287

Sequence: 1 gacatctccgtttccctccc.....aaagtttaactgactatatg 1287

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 segs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : GenEmbl:*

1: gb_env:*

2: gb_pat:*

3: gb_ph:*

4: gb_pl:*

5: gb pr:*

6: gb_ro:*

7: gb_sts:*

8: gb_sy:*

9: gb_un:* 10: gb_vi:*

11: gb_ov:*

12: gb_htg:*

13: gb_in:*

14: gb om:*

15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			*5				
I	Result No.	Score	Query Match	Length	DB	ID	Description
	1	1287	100.0	1287	2	CQ850430	CQ850430 Sequence
	2	1287	100.0	1287	5	AK127564	AK127564 Homo sapi
	3	1283.8	99.8	1370	5	BC073975	BC073975 Homo sapi
	4	1062.2	82.5	1496	5	BC016167	BC016167 Homo sapi
	5	1062.2	82.5	1556	5	BC064397	BC064397 Homo sapi
	6	943.4	73.3	1246	14	BC109937	BC109937 Bos tauru
	7	721.2	56.0	1202	6	BC088194	BC088194 Rattus no
	8	588.8	45.7	893	6	BC100355	BC100355 Mus muscu
	9	487.8	37.9	179531	14	CR933563	CR933563 Wallaby D
	10	474	36.8	546	2	CQ722465	CQ722465 Sequence
	11	405.2	31.5	29862	5	AL662798	AL662798 Human DNA
	12	405.2	31.5	39659	12	CR847874	CR847874 Homo sapi
	13	405.2	31.5	71418	5	AL732442	AL732442 Human DNA
	14	405.2	31.5	88815	5	CR759778	CR759778 Human DNA
	15	405.2	31.5	104755	5	BX908728	BX908728 Human DNA
	16	405.2	31.5	105135	5	CR753328	CR753328 Human DNA
	c 17	405.2	31.5	110000	5	BA000025 12	Continuation (13 o
	c 18	405.2	31.5	110000	5	BA000041 08	Continuation (9 of
	19	405.2	31.5	112118	5	BX119957	BX119957 Human DNA
	c 20	405.2	31.5	123554	5	AB023049	AB023049 Homo sapi

```
31.5 130755 5 AL845353
                                                          AL845353 Human DNA
        405.2
                31.5 151228
                             5 AL662800
                                                          AL662800 Human DNA
   23
                31.5 310542 12 CR752729
                                                          CR752729 Homo sapi
        405.2
                31.5 349980 2 CS039417
                                                          CS039417 Sequence
   25
          396
                30.8
                        404 2 AX070414
                                                          AX070414 Sequence
        395.6
                30.7 110000 5 AB128049 17
                                                          Continuation (18 o
   27
                30.7 174766 5 AC148659
        395.6
                                                          AC148659 Macaca mu
          335
                26.0 114375
                             14 AB113357
                                                          AB113357 Sus scrof
                26.0 146382 14 AB113356
          335
                                                          AB113356 Sus scrof
   30
        325.2
                25.3
                        473 2 AX982153
                                                          AX982153 Sequence
                        473 2 BD117012
473 2 AR421459
   31
        325.2
                25.3
                                                          BD117012 EST and e
   32
        325.2
                25.3
                                                          AR421459 Sequence
          302
                23.5
                        634 7 BV238118
                                                          BV238118 S234P6240
        300.8
                        504 6 BC058418
437 2 AX335791
   34
                23.4
                                                          BC058418 Mus muscu
С
        286.8
                22.3
                                                          AX335791 Sequence
                        437 2 AX409947
   36
        286.8
                22.3
                                                          AX409947 Sequence
                22.2 153274 12 AY555280
                                                          AY555280 Mus muscu
   38
                21.9 172747 6 AC112970
        282.4
                                                          AC112970 Mus muscu
        282.4
                21.9 188873 6 CR974451
                                                          CR974451 Mouse DNA
        273.8
                21.3
                        300 2 BD219935
                                                          BD219935 Human gen
                20.9 349980 2 AX344571
   41
        269.4
                                                          AX344571 Sequence
        269.4
                20.9 349980
                             2 AX344572
                                                          AX344572 Sequence
                19.7 297409 12 AC096275
   43
        253.2
                                                           AC096275 Rattus no
                19.7 349943 6 BX883048
                                                          BX883048 Rattus no
  45
          229
                17.8 21070 5 AB202095
                                                          AB202095 Homo sapi
          229
                17.8 21071 5
                                AB088098
                                                          AB088098 Homo sapi
                        192 2 AX905901
   47
        189.6
                14.7
                                                          AX905901 Sequence
                        192 2 BD041434
        189.6
                14.7
                                                          BD041434 Sequence
                                                          AR741695 Sequence
        189.6
                14.7
                        192 2
                                AR741695
        175.6
                13.6 349980 2
                                AX344552
                                                          AX344552 Sequence
<!--EndFragment-->
```

```
<!--StartFragment-->GenCore version 5.1.9
                  Copyright (c) 1993 - 2006 Biocceleration Ltd.
OM nucleic - nucleic search, using sw model
                November 3, 2006, 13:59:52; Search time 918 Seconds
                                            (without alignments)
                                           9774.819 Million cell updates/sec
Title:
                US-10-777-288A-899
Perfect score: 1287
Sequence:
                1 gacatctccgtttccctccc.....aaagtttaactgactatatg 1287
Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0
Searched:
                5244920 segs, 3486124231 residues
Total number of hits satisfying chosen parameters:
                                                        10489840
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                Maximum Match 100%
                 Listing first 300 summaries
Database :
                N_Geneseq_8:*
                1: geneseqn1980s:*
                2: geneseqn1990s:*
                3: geneseqn2000s:*
4: geneseqn2001as:*
                5: geneseqn2001bs:*
                6: geneseqn2002as:*
                7: geneseqn2002bs:*
                8: geneseqn2003as:*
                9: geneseqn2003bs:*
                10: geneseqn2003cs:*
                11: geneseqn2003ds:*
                12: geneseqn2004as:*
                13: geneseqn2004bs:*
                14:
                    geneseqn2005s:*
                15: geneseqn2006s:*
      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
```

and is derived by analysis of the total score distribution.

Result No.		Score	Query Match	Length	DB	ID	Description
	1	1287	100.0	1287	13	ADR07393	Adr07393 Full leng
2		1219.8	94.8	1223	12	ADQ87293	Adq87293 Human tum
	3	1219.8	94.8	1223	12	ADQ83838	Adq83838 Human tum
	4	1059.6	82.3	1243	8	ABX05085	Abx05085 Human nov
	5	443.8	34.5	591	13	ADQ53687	Adq53687 Novel can
	6	396	30.8	404	5	AAF65130	Aaf65130 Novel hum
	7	392	30.5	400	9	ACH16377	Ach16377 Human adu
С	8	298.8	23.2	2036	4	AAD05547	Aad05547 Human sec
	9	296.6	23.0	491	14	ADZ61349	Adz61349 Rat g2936
С	10	286.8	22.3	437	6	ABL67963	Abl67963 Ovary can
С	11	286.8	22.3	437	6	ABN96096	Abn96096 Gene #259
С	12	279.8	21.7	457	10	ABT41359	Abt41359 Toxicity
	13	273.8	21.3	300	3	AAA01057	Aaa01057 Human col
	14	189.6	14.7	192	3	AAC17689	Aac17689 Human sec
С	15	117	9.1	644	5	AAS34255	Aas34255 Human cDN
С	16	70.4	5.5	3133	10	ADC86738	Adc86738 Human GPC
С	17	69.2	5.4	629	13	ACN54594	Acn54594 Cotton an
С	18	69	5.4	3163	10	ADC87060	Adc87060 Human GPC
	19	68.8	5.3	28198	10	ADG37080	Adg37080 Mouse pla
	20	68.4	5.3	563	5	AAS34384	Aas34384 Human cDN

С	21	66	5.1	5452	10	ADC86736	Adc86736 Human GP0
С	22	65.2	5.1	12733	6	ABK98631	Abk98631 Vector pE
С	23	65.2	5.1	12733	9	ACD13882	Acd13882 L. lactis
С	24	65.2	5.1	12739	6	ABK98592	Abk98592 Vector pE
C	25	65.2	5.1	12739	9	ACD13843	Acd13843 Plasmid p
С	26	65	5.1	1117	10	ADC86688	Adc86688 Human GPC
С	27	64	5.0	588	13	ACN54596	Acn54596 Cotton ar
	28	64	5.0	1064	6	ABT09678	Abt09678 Human PAL
	29	62	4.8	500	12	ADP85918	Adp85918 Synthetic
С	30	60.2	4.7	40772	13	ADW39403	Adw39403 Herpes si
С	31	60	4.7	1000	3	AAA02484	Aaa02484 Human col
	32	58.8	4.6	1337	2	AAZ17263	Aaz17263 Human gen
С	33	58.4	4.5	931	11	ACN87435	Acn87435 Breast ca
	34	58.4	4.5	1065	6	ABT09682	Abt09682 Human PAL
	35	57.4	4.5	600	6	ABQ52497	Abg52497 Oligonucl
С	36	57.4	4.5	600	6	ABQ52496	Abq52496 Oligonucl
С	37	57.4	4.5	1459	3	AAA02528	Aaa02528 Human col
	38	56.4	4.4	406	13	ACN59490	Acn59490 Cotton gy
	39	56.2	4.4	53522	6	AAD30228	Aad30228 Human PKD
	40	56.2	4.4	53522	13	ADU03973	Adu03973 Human pol
	41	56.2	4.4	53522	14	AEB35216	Aeb35216 Human Gei
	42	56.2	4.4	53526	2	AAT94101	Aat94101 Human PKD
	43	56.2	4.4	53577	2	AAT18551	Aat18551 Human pol
	44	56.2	4.4	53577	2	AAT94108	Aat94108 Human PKD
	45	56	4.4	4897	2	AAQ03259	Aaq03259 Pseudorab
С	46	55.2	4.3	1416	8	ABZ20967	Abz20967 Animal te
	47	55	4.3	987	6	ABT09669	Abt09669 Human PAL
С	48	54.6	4.2	795	2	AAV55830	Aav55830 FLGA inse
	49	54	4.2	478	13	ACN51281	Acn51281 Cotton ar
С	50	54	4.2	799	2	AAV55831	Aav55831 Nucleotid
-</td <td>-End</td> <td>Fragment-</td> <td>-></td> <td></td> <td></td> <td></td> <td></td>	-End	Fragment-	->				

```
<!--StartFragment-->GenCore version 5.1.9
                  Copyright (c) 1993 - 2006 Biocceleration Ltd.
OM nucleic - nucleic search, using sw model
Run on:
                November 3, 2006, 14:10:30 ; Search time 6938 Seconds
                                           (without alignments)
                                           10373.044 Million cell updates/sec
                US-10-777-288A-899
Title:
Perfect score:
                1287
Sequence:
                1 gacatctccgtttccctccc.....aaagtttaactgactatatg 1287
Scoring table: IDENTITY NUC
                Gapop 10.0 , Gapext 1.0
Searched:
                48236798 seqs, 27959665780 residues
Total number of hits satisfying chosen parameters:
                                                        96473596
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                Maximum Match 100%
                Listing first 300 summaries
                EST:*
Database :
                1: gb_est1:*
                2: gb_est3:*
                3: gb_est4:*
                4: gb_est5:*
                5: gb_est6:*
                6: gb htc:*
                7: gb_est2:*
                8: gb_est7:*
                9: gb_est8:*
                10: gb est9:*
                11: gb_gss1:*
                    gb_gss2:*
                12:
                13:
                    gb_gss3:*
                14:
                    gb_gss4:*
     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.
```

Result No.		Score	Query Match	Length	DB	ID	Description
 c	1	883	68.6	985	4	BX340635	BX340635 BX340635
	2	872.8	67.8	876	14	DQ054028	DQ054028 Homo sapi
	3	854.2	66.4	876	14	DQ054029	DQ054029 Pan trogl
	4	846	65.7	1094	3	BM558827	BM558827 AGENCOURT
	5	796.8	61.9	1060	2	BM551645	BM551645 AGENCOURT
	6	730.4	56.8	915	3	BQ954823	BQ954823 AGENCOURT
	7	724.2	56.3	1097	3	BM926246	BM926246 AGENCOURT
	8	721.8	56.1	869	3	BP165929	BP165929 BP165929
	9	709.8	55.2	1288	6	AK145087	AK145087 Mus muscu
	10	709.4	55.1	1151	6	AK172070	AK172070 Mus muscu
	11	702.4	54.6	2082	6	AK038622	AK038622 Mus muscu
	12	675	52.4	675	9	DR157885	DR157885 HESC2_83_
С	13	674.8	52.4	739	3	BM677371	BM677371 UI-E-E01-
	14	656.2	51.0	694	2	BI765223	BI765223 603050308
С	15	649.4	50.5	662	7	BF221823	BF221823 7p37b09.x
	16	628.6	48.8	669	2	BI763966	BI763966 603049847
С	17	626.2	48.7	679	7	BF224092	BF224092 7q83g03.x
	18	625.8	48.6	820	9	DN107093	DN107093 1104510 M
С	19	623.8	48.5	819	9	DN106729	DN106729 1104126 M
	20	610.6	47.4		10	DT837916	DT837916 LB00441.C
	21	608.8	47.3	746	9	DN871473	DN871473 nad13f12.

	22	594.4	46.2	742	8	CO889119	CO889119 BovGen_17
С	23	589.8	45.8	612	3	BU679422	BU679422 UI-CF-DU1
	24	587.2	45.6	667	2	BI764214	BI764214 603046086
C	25	578.2	44.9	781	9	CX991484	CX991484 DOG_EST_P
	26	576	44.8	576	5	CK825958	CK825958 ik36f08.x
	27	571	44.4	571	9	DA444680	DA444680 DA444680
	28	570.2	44.3	739	6	AY610091	AY610091 Sus scrof
	29	559.8	43.5	806	8	CX218593	CX218593 MNS33196
С	30	550.4	42.8	595	5	CK825959	CK825959 ik36f08.y
	31	546.2	42.4	892	5	CF617102	CF617102 AGENCOURT
	32	546	42.4	976	3	BU513239	BU513239 AGENCOURT
С	33	544	42.3	544	9	DB313908	DB313908 DB313908
С	34	541.2	42.1	749	4	CB321830	CB321830 UI-CF-EN1
	35	535.4	41.6	595	7	AW967384	AW967384 EST379459
	36	535.4	41.6	668	5	CF358996	CF358996 818572 MA
	37	533	41.4	908	5	CF618737	CF618737 AGENCOURT
	38	530	41.2	720	10	DT719601	DT719601 LB0111.CF
	39	526.8	40.9	644	5	CK956234	CK956234 4096335 B
	40	523.8	40.7	527	3	BQ417335	BQ417335 ik36f08.y
	41	521	40.5	521	3	BM790196	BM790196 K-EST0069
С	42	515.4	40.0	518	1	AI143133	AI143133 qb76d09.x
	43	514.2	40.0	627	2	BI837701	BI837701 603086558
	44	512	39.8	773	8	CX239247	CX239247 NMA07043
	45	511.8	39.8	842	4	CA459080	CA459080 AGENCOURT
	46	510.2	39.6	649	5	CK946125	CK946125 4070565 B
	47	. 509	39.5	631	8	CO894259	CO894259 BovGen_22
	48	507.6	39.4	514	5	CD674180	$CD674180 fs07e1\overline{2}.y$
	49	504.6	39.2	860	8	CX200108	CX200108 MNS00694
С	50	502	39.0	510	7	BF590482	BF590482 7h35g05.x
-</td <td>-End</td> <td>Fragment-</td> <td>></td> <td></td> <td></td> <td></td> <td></td>	-End	Fragment-	>				

```
<!--StartFragment-->GenCore version 5.1.9
                  Copyright (c) 1993 - 2006 Biocceleration Ltd.
OM nucleic - protein search, using frame_plus_n2p model
                November 3, 2006, 14:33:07; Search time 46.7 Seconds
                                             (without alignments)
                                             3780.113 Million cell updates/sec
                US-10-777-288A-899
Title:
Perfect score: 2348
Sequence:
                1 gacatctccgtttccctccc.....aaagtttaactgactatatg 1287
Scoring table: BLOSUM62
                Xgapop 10.0 , Xgapext 0.5
                Ygapop 10.0 , Ygapext 0.5
                Fgapop 6.0 , Fgapext 7.0 Delop 6.0 , Delext 7.0
Searched:
                2589679 seqs, 457216429 residues
Total number of hits satisfying chosen parameters: 5179358
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 300 summaries
Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10777288/runat_03112006_105409_8336/app_query.fasta_1
-DB=A Geneseq -QFMT=fastan -SUFFIX=n2p.100aligns.rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=300 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=100
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss02p -USER=US10777288 @CGN_1_1_364 @runat_03112006_105409_8336
-NCPU=6 -ICPU=3 -NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                A Geneseq 8:*
                1: geneseqp1980s:*
                 2: geneseqp1990s:*
                3: geneseqp2000s:*
4: geneseqp2001s:*
                 5: geneseqp2002s:*
                 6: geneseqp2003as:*
                 7: geneseqp2003bs:*
                 8: geneseqp2004s:*
                 9: geneseqp2005s:*
                 10: geneseqp2006s:*
      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.
                                      SUMMARIES
                 용
Result
                 Query
        Score Match Length DB ID
                                                              Description
   No.
  1728 73.6 315 8 ADR09349
907 38.6 172 6 ABG99987
                                                              Adr09349 Human pro
     1
                                                              Abg99987 Human nov
     2
                10.4 238 4 ABB68306
         243.5
                                                             Abb68306 Drosophil
                 10.2 598 4 ABG14000
10.2 598 7 ADF60423
          240
                                                             Abg14000 Novel hum
     4
     5
           240
                                                              Adf60423 Human con
                  9.3 1216 8 ADX97588
                                                             Adx97588 Pancreati
         219.5
     7
         219.5
                 9.3 1250 6 AAO26231
                                                             Aao26231 MDDT rela
```

219.5 9.3 1250 8 ADM87156 209 8.9 763 2 AAW31852

8.8 693 7 ADM05164

8

9

207.5

Adm87156 Human pro

Aaw31852 Mycobacte

Adm05164 Human pro

11 207.5 8.8 693 9 AEC88094 Aec88094 Human CDI 12 204.5 8.7 693 5 ABP69529 Abp69529 Human pol 13 203.5 8.7 1008 4 ABB1527 Abb1527 Human app 14 200 8.5 406 4 ABG27250 Abg27250 Novel hur 15 199 8.5 446 4 ABB70063 Abb70063 Crosophi- 16 199 8.5 1579 8 ADS97981 Ads97981 Protein: 17 199 8.5 2161 7 ADJ69477 Adj69477 Human her 18 199 8.5 2161 9 ADX98562 Adx98562 Human SRI 19 198.5 8.5 598 6 ABU37030 Abu37030 Protein c 20 198.5 8.5 598 6 ABU37030 Abu37030 Protein c 21 198 8.4 572 2 AAW31855 Aaw31855 Mycobacte 22 196.5 8.4 313 8 AB059570 Abo59570 Human ger 23 193.5 8.2 1315 2 AAW76734 Aaw76734 Human mb. 24 193.5 8.2 1315 2 AAW76734 Aaw76734 Human mb. 24 193.5 8.2 1616 8 ADP22958 Adp22958 PRO poly 25 192 8.2 800 8 AB058864 Abo58564 Human ger 26 191.5 8.2 1567 7 ABW01569 Abw01569 Mouse for 28 191.5 8.2 1567 7 ABW01569 Abw01569 Mouse for 28 191.5 8.2 1682 8 ADR14131 Adr14131 Human Nb. 30 191 8.1 451 7 ADE62342 Adc24242 Rat Prote 31 190 8.1 639 8 ADN21309 Adn21309 Bacterial 32 188.5 8.0 681 5 ABB93650 Abb93650 Abb93650 Herbicidal c 33 188.5 8.0 684 4 ABG14126 Abg14126 Novel hur 34 187.5 8.0 1006 8 ADU20559 Adu20559 A. thalic 36 187.5 8.0 1006 8 ADU20559 Adu20559 A. thalic 36 187.5 8.0 1006 8 ADU20559 Adu20559 A. Lhalic 39 185.5 7.9 280 7 ABW01569 Abb93650 Herbicidal 30 186.7 7.9 694 5 ABB92421 Abb92421 Herbicidal 30 185.5 7.9 280 7 ABW01569 Abc366 Abb03668 Mouse for 31 187 8.0 1413 5 AAE21729 Aae21729 Human PKI 38 186.7 7.9 694 5 ABB92421 Abb92421 Herbicidal 39 185.5 7.9 280 7 ABW01569 Abc366 Abw01568 Mouse for 40 183 7.8 325 4 ABG21919 Abg21919 Novel hur 41 183 7.8 386 9 ADZ47759 AdZ47759 AdZ47759 Mycobacte 42 183 7.7 707 9 ADE34941 Abe31351 Human PKI 48 180.5 7.7 707 7 ADE54938 Abc34941 Human PKI 48 180.5 7.7 707 7 ADE54938 Human PKI 48 180.5 7.7 707 7 ADE54938 Human PKI									
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44 181 7.7 707 9 ADZ44698 Adz44698 NFk-B pro 45 181 7.7 707 9 AEB31351 Aeb31351 Human PSI 46 180.5 7.7 525 9 AEB31354 Aeb31354 Human SFI 47 180.5 7.7 669 9 AEB31352 Aeb31352 Human PSI 48 180.5 7.7 707 4 AAM39141 Aam39141 Human Pro 49 180.5 7.7 707 7 ADE54941 Ade54941 Human Pro 50 180.5 7.7 707 7 ADE54938 Ade54938 Human Pro		43	182.5	7.8	1313	7	ADJ70374		
45 181 7.7 707 9 AEB31351 Aeb31351 Human PSI 46 180.5 7.7 525 9 AEB31354 Aeb31354 Human SFI 47 180.5 7.7 669 9 AEB31352 Aeb31352 Human PSI 48 180.5 7.7 707 4 AAM39141 Aam39141 Human Pol 49 180.5 7.7 707 7 ADE54941 Ade54941 Human Pro 50 180.5 7.7 707 7 ADE54938 Ade54938 Human Pro		44		7.7		9		Adz44698	NFk-B pro
46 180.5 7.7 525 9 AEB31354 Aeb31354 Human SFI 47 180.5 7.7 669 9 AEB31352 Aeb31352 Human PSI 48 180.5 7.7 707 4 AAM39141 Aam39141 Human Pro 49 180.5 7.7 707 7 ADE54941 Ade54941 Human Pro 50 180.5 7.7 707 7 ADE54938 Ade54938 Human Pro		45	181	7.7	707	9			
47 180.5 7.7 669 9 AEB31352 Aeb31352 Human PSI 48 180.5 7.7 707 4 AAM39141 Aam39141 Human PSI 49 180.5 7.7 707 7 ADE54941 Ade54941 Human Pro 50 180.5 7.7 707 7 ADE54938 Ade54938 Human Pro		46	180.5	7.7	525	9			
48 180.5 7.7 707 4 AAM39141 Aam39141 Human pol 49 180.5 7.7 707 7 ADE54941 Ade54941 Human Pro 50 180.5 7.7 707 7 ADE54938 Ade54938 Human Pro		47	180.5	7.7	669	9	AEB31352		
49 180.5 7.7 707 7 ADE54941 Ade54941 Human Pro 50 180.5 7.7 707 7 ADE54938 Ade54938 Human Pro		48							
50 180.5 7.7 707 7 ADE54938 Ade54938 Human Pro		49				7			
	<b --	-EndF		>					

```
<!--StartFragment-->
                              GenCore version 5.1.9
                   Copyright (c) 1993 - 2006 Biocceleration Ltd.
OM nucleic - protein search, using frame_plus_n2p model
Run on:
                 November 3, 2006, 14:44:57; Search time 11.1 Seconds
                                             (without alignments)
                                             3346.783 Million cell updates/sec
Title:
                 US-10-777-288A-899
Perfect score:
                2348
Sequence:
                 1 gacatctccgtttccctccc.....aaagtttaactgactatatg 1287
Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext
                 Delop
                         6.0 , Delext
Searched:
                 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters:
                                                           566832
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 300 summaries
Command line parameters:
-MODEL=frame+_n2p.model -DEV=x1p
-Q=/abss/ABSSWEB spool/US10777288/runat 03112006 105413 8382/app query.fasta 1
-DB=PIR -QFMT=fastan -SUFFIX=n2p.100aligns.rpr -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=300 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=100
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss02p -USER=US10777288_@CGN_1_1_71_@runat_03112006_105413_8382 -NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                PIR_80:*
Database :
                 1: pir1:*
                 2: pir2:*
                    pir3:*
                3:
                 4: pir4:*
      Pred. No. is the number of results predicted by chance to have a
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			8				
Result			Query				
	No.	Score Match		Length	DB	ID	Description
	1	203.5	8.7	. 839	2	T04859	extensin homolog F
	2	190.5	8.1	577	2	T09024	proline-rich prote
	3	187.5	8.0	1006	2	G86292	hypothetical prote
	4	185.5	7.9	1690	2	Т31670	DNA-directed RNA p
	5	181.5	7.7	530	2	A45690	transactivator EBN
C	6	181.5	7.7	682	2	T28899	hypothetical prote
	7	181	7.7	990	2	T14756	hypothetical prote
	8	180.5	7.7	707	2	A46302	PTB-associated spl
	9	180	7.7	416	2	T34279	hypothetical prote
	10	180	7.7	1184	2	G01763	atrophin-1 - human
С	11	179.5	7.6	274	2	T25404	hypothetical prote
	12	179	7.6	464	2	S22697	extensin - Volvox
	13	178	7.6	376	2	S71558	probable cell wall
	14	178	7.6	1184	2	S50832	atrophin-1 - human
С	15	177.5	7.6	375	2	JS0427	S-antigen precurso

	16	176.5	7.5	786	2	T01456
	17	176.5	7.5	1255	2	T31065
	18	176	7.5	473	2	S50755
	19	176	7.5	708	2	D96711
	20	174.5	7.4	1188	2	S49915
	21	174	7.4	1357	2	T29265
С	22	173	7.4	1549	2	I48103
	23	172	7.3	1494	2	T14355
	24	171.5	7.3	350	2	S22456
	25	171.5	7.3	1611	2	T38236
	26	171	7.3	666	2	B70803
	27	171	7.3	1541	2	T02831
	28	170	7.2	620	2	S06733
С	29	170	7.2	1489	2	D70807
	30	170	7.2	3020	2	A43932
	31	169.5	7.2	1520	2	T00273
	32	169	7.2	439	2	S51939
	33	169	7.2	760	2	F86387
	34	169	7.2	907	2	E96636
	35	168.5	7.2	306	2	T52340
	36	168	7.2	515	2	F70904
	37	167.5	7.1	548	2	S59133
С	38	167.5	7.1	1660	2	A70869
	39	167.5	7.1	1859	1	A34092
	40	167.5	7.1	1862	2	T29959
	41	167	7.1	449	2	S16748
	42	167	7.1	915	2	T12526
	43	167	7.1	5262	2	T03454
С	44	166.5	7.1	346	1	S35500
С	45	166.5	7.1	584	2	G70804
	46	165.5	7.0	839	2	F75518
	47	165.5	7.0	4957	2	T03455
	48	165	7.0	487	2	S42442
	49	165	7.0	744	2	E86255
					_	

1201

2

G86441

extensin homolog F diaphanous protein hypothetical prote hypothetical prote extensin-like prot hypothetical prote type VII collagen protein-tyrosine-p hydroxyproline-ric hypothetical prote hypothetical prote AAA protein L4171. hydroxyproline-ric hypothetical glyci mucin 2 precursor, hypothetical prote chitinase (EC 3.2. probable Pto kinas hypothetical prote cell wall-plasma m hypothetical prote ETS2 repressor fac hypothetical glyci DNA-directed RNA p DNA-directed RNA p proline-rich prote hypothetical prote ALR protein - huma heterogeneous ribo hypothetical glyci hypothetical prote ALR protein - huma nuclear protein EB hypothetical prote unknow<!--EndFragment-->

```
<!--StartFragment--> GenCore version 5.1.9
                   Copyright (c) 1993 - 2006 Biocceleration Ltd.
OM nucleic - protein search, using frame_plus_n2p model
                November 3, 2006, 14:34:27; Search time 83 Seconds
                                              (without alignments)
                                             4302.994 Million cell updates/sec
                US-10-777-288A-899
Title:
Perfect score: 2348
Sequence:
                1 gacatctccgtttccctccc.....aaagtttaactgactatatg 1287
Scoring table: BLOSUM62
                Xgapop 10.0 , Xgapext 0.5
                Ygapop 10.0 , Ygapext 0.5
                Fgapop 6.0 , Fgapext Delop 6.0 , Delext
                                         7.0
Searched:
                2849598 seqs, 925015592 residues
Total number of hits satisfying chosen parameters:
                                                           5699196
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 300 summaries
Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10777288/runat_03112006_105411_8347/app_query.fasta_1
-DB=UniProt -QFMT=fastan -SUFFIX=n2p.100aligns.rup -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=300 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=100
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss02p -USER=US10777288_@CGN_1_1_684_@runat_03112006_105411_8347 -NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                UniProt_7.2:*
Database :
                1: uniprot_sprot:*
                2: uniprot_trembl:*
      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
```

and is derived by analysis of the total score distribution.

			8				
Re	sult		Query				
	No.	Score	Match	Length	DB	ID	Description
	1	1716	73.1	315	1	CF136_HUMAN	Q5sqh8 homo sapien
	2	1519	64.7	315	2	Q32KT5_BOVIN	Q32kt5 bos taurus
	3	1267	54.0	338	2	Q3UM69 MOUSE	Q3um69 mus musculu
	4	1256	53.5	326	2	Q3TA61 MOUSE	Q3ta61 mus musculu
	5	880	37.5	172	1	CF136 MACMU	Q5tm64 macaca mula
	6	792	33.7	172	1	CF136 RAT	Q6mg12 rattus norv
	7	788	33.6	172	2	Q497V8_MOUSE	Q497v8 mus musculu
	8	476	20.3	102	2	Q6PDX4 MOUSE	Q6pdx4 mus musculu
	9	441	18.8	178	2	Q5PPL5_XENTR	Q5ppl5 xenopus tro
	10	285.5	12.2	247	2	Q7PFX4_ANOGA	Q7pfx4 anopheles g
	11	243.5	10.4	253	2	Q9W1F2_DROME	Q9w1f2 drosophila
	12	239.5	10.2	253	2	Q8SYW2_DROME	Q8syw2 drosophila
	13	234.5	10.0	3409	2	Q6SSE6_CHLRE	Q6sse6 chlamydomon
	14	225	9.6	3889	2	Q6SSE8_CHLRE	Q6sse8 chlamydomon
	15	219.5	9.3	1302	1	RAPH1_HUMAN	Q70e73 homo sapien
•	16	217.5	9.3	4027	2	Q5I2RO_CHLIN	Q5i2r0 chlamydomon
	17	217	9.2	2371	2	Q58NA5_CHLIN	Q58na5 chlamydomon
	18	212.5	9.1	2332	2	Q4A2B5_9PHYC	Q4a2b5 emiliania h

	19	212	9.0	555	1	GP1_CHLRE	Q9fpq6	chlamydomon
	20	210.5	9.0	1332	2	Q59GF6_HUMAN	Q59gf6	homo sapien
	21	210.5	9.0	1865	2	Q5VU37 HUMAN	Q5vu37	homo sapien
	22	210	8.9	665	2	Q2U6Q3_ASPOR		aspergillus
	23	209	8.9	763	2	Q9XDH2 MYCTU	Q9xdh2	mycobacteri
	24	207.5	8.8	585	2	O41935 MHV68	041935	murid herpe
	25	206.5	8.8	727	2	Q35LL9 9BRAD		bradyrhizob
	26	206.5	8.8	745	2	Q89X06 BRAJA	Q89x06	bradyrhizob
	27	206	8.8	516	2	Q4A2Z7 9PHYC	Q4a2z7	emiliania h
	28	204.5	8.7	616	2	Q9H6K5 HUMAN	Q9h6k5	homo sapien
	29	203.5	8.7	839	2	Q9SN46 ARATH		arabidopsis
	30	201.5	8.6	861	2	Q69JZ8 ORYSA		oryza sativ
	31	199	8.5	420	2	Q9VZC2_DROME	Q9vzc2	drosophila
	32	199	8.5	2161	1	SHAN1 HUMAN	Q9y566	homo sapien
	33	198.5	8.5	598	2	Q8VKN7 MYCTU	Q8vkn7	mycobacteri
	34	198.5	8.5	676	2	Q95JC9_PIG	Q95jc9	sus scrofa
	35	197.5	8.4	498	2	Q5KGJ5 CRYNE	Q5kgj5	cryptococcu
	36	197	8.4	946	2	Q2R063 ORYSA	Q2r063	oryza sativ
	37	197	8.4	2033	2	Q9E938 9ALPH	Q9e938	gallid herp
	38	197	8.4	2033	2	Q9E940 9ALPH	Q9e940	gallid herp
	39	195	8.3	3204	2	Q6X248_9ALPH	Q6x248	bovine herp
	40	193.5	8.2	511	2	Q95JD0_PIG	Q95jd0	sus scrofa
	41	193.5	8.2	566	2	Q95JD1_PIG	Q95jd1	sus scrofa
	42	193.5	8.2	687	2	Q948Y7_VOLCA		volvox cart
	43	193.5	8.2	1272	2	Q6URC4 HUMAN	Q6urc4	homo sapien
	44	193.5	8.2	1299	2	Q59FH8_HUMAN	Q59fh8	homo sapien
	45	191.5	8.2	410	2	Q7PZX2_ANOGA	Q7pzx2	anopheles g
	46	191.5	8.2	1248	1	DIAP1_HUMAN	060610	homo sapien
	47	191.5	8.2	1567	1	FMN2 MOUSE	Q9j104	mus musculu
	48	191.5	8.2	1682	2	015054 HUMAN	015054	homo sapien
	49	191	8.1	309	2	Q8UZB4_9VIRU		grapevine f
	50	191	8.1	451	2	Q62775_RAT	Q62775	rattus norv
! –	-EndF	ragment	>			_		1